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Typed or printed name of person signing this certificate:



24024

PATENT TRADEMARK OFFICE

Signed: Candice Moore

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of	)	Examiner: Not yet assigned
Gorski, et al.	)	
Serial No.: Not yet assigned	)	Group Art Unit: Not yet assigned
Parent Serial Number: 09/078,465	)	
Filed: Concurrently herewith	)	
Parent Filed: May 14, 1998	)	
For: <b>GROWTH ARREST HOMEBOX</b>	)	Attorney Docket No.: 22311/04015
<b>GENE</b>	)	

Assistant Commissioner for Patents  
Washington, D.C. 20231

FIRST PRELIMINARY AMENDMENT

Dear Sir:

Please amend the above-identified continuation application as follows:

In the Specification:

Page 1, before "Background of the Invention" insert

Cross-Reference to Related Applications

This application is a continuation of the co-pending, commonly assigned, United States Patent Application Serial No.: 09/078,465, filed on May 14, 1998, which is a continuation of United States Application Serial No. 08/203,532, filed on February 24, 1994, and which issued as U.S. Patent No. 5,856,121 on January 5, 1999.

Page 1, line 21, delete "extra cellular" and insert ---extracellular---

Page 2, lines 23 to 24, delete "extra cellular" and insert ---extracellular---

Page 3, line 14, delete "the".

Page 3, line 15, delete "The".

Page 4, line 6, after "sequence" add ---SEQ ID NO: 1---

Page 4, line 7, after "sequence" add ---SEQ ID NO: 2---

Page 4, line 20, after "sequence" add ---SEQ ID NO: 3---

Page 4, line 21, after "sequence" add --- SEQ ID NO: 4 ---.

Page 7, line 16, delete "nucleotide" and insert ---nucleotide---

Page 8, line 9, after "sequence" add --- SEQ ID NO: 5---

Page 8, line 36, after "gene" add ---SEQ ID NO: 1---

Page 9, line 9, after "protein" add --- SEQ ID NO: 2---

Page 9, line 19, delete the word "phosphorylated".

Page 12, line 20, after "sequence" add ---SEQ ID NO: 3---

Page 15, lines 2 and 3, delete the word "follows".

Page 16, line 6, after "P2B" add ---SEQ ID NO: 6---

Page 16, line 7, after "H2" add ---SEQ ID NO: 7---

Page 16, line 8, after "H2R" add ---SEQ ID NO: 8---

Page 16, line 9, after "H3" add ---SEQ ID NO: 9---

Page 16, line 10, after "H6" add ---SEQ ID NO: 10---

Page 16, line 11, after "H7" add ---SEQ ID NO: 11---

Page 16, line 12, after "AP" add ---SEQ ID NO: 12---

Page 16, line 13, after "Anchor" add ---SEQ ID NO: 13---

Page 18, line 16, delete "bank" and insert ---band---. Id.

Page 22, line 26, after "3" insert ---SEQ ID NO: 14---

Page 22, line 27, after "3" add ---SEQ ID NO: 15---

Page 23, line 37, delete "6752," and insert ---6762.---

Page 29, line 1, delete "The".

page 31, line 16, delete "oligo sequence" and insert ---oligosequence---

Page 31, line 19, after "3" add ---SEQ ID NO: 16---

Page 31, line 20, after "3" add ---SEQ ID NO: 17---

Page 31, line 21, after "3" add ---SEQ ID NO: 18---

Page 31, line 22, after “3” add ---SEQ ID NO: 19---

Page 33, please replace the Sequence Listing with the Sequence Listing which is attached hereto.

#### IN THE CLAIMS

Please amend the claims as follows:

1. (Amended) An isolated DNA encoding a mammalian Gax protein [or portion thereof] which inhibits vascular smooth muscle cell proliferation, said Gax protein having a molecular weight of about 30 to 36kDa and comprising a homeodomain, wherein the amino acid sequence of said homeodomain comprises amino acid 185 through amino acid 245 of the amino acid sequence set forth in SEQ. ID. NO. 4.

Please cancel claims 2-4, 6-12, 14-17, 19-22, 24-27 and 29-32 without prejudice or disclaimer.

Please add the following claims:

33. (New) An isolated nucleic acid molecule comprising a nucleotide sequence encoding a Gax protein that inhibits vascular smooth muscle cell proliferation, said Gax protein having an amino acid sequence consisting essentially of the amino acid sequence set forth in SEQ. ID. NO. 2 or the amino acid sequence set forth in SEQ. ID. NO. 4.

34. (New) An isolated nucleic acid molecule encoding a Gax protein that inhibits vascular smooth muscle cell proliferation, said nucleic acid molecule comprising a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the following:

- (a) amino acid 223 through amino acid 302 of the sequence set forth in SEQ. ID. NO. 4;
- (b) amino acid 67 through amino acid 222 of the sequence set forth in SEQ. ID. NO. 4;
- (c) amino acid 30 through amino acid 66 of the sequence set forth in SEQ. ID. NO. 4;
- (d) amino acid 1 through amino acid 29 of the sequence set forth in SEQ. ID. NO. 4; and

combinations thereof.

35. (New) The isolated nucleic acid molecule of claim 34 wherein said Gax protein has a molecular weight of from about 30 kDa to about 36 kDa.

36. (New) A process for preparing an isolated nucleic acid molecule encoding a Gax protein that inhibits vascular smooth muscle cell proliferation comprising the following steps:

(a) providing a human cDNA library which comprises a cDNA molecule encoding a Gax protein;

(b) amplifying said cDNA molecule by a polymerase chain reaction using said cDNA molecule as a template and a pair of primers which bind under stringent conditions to the 5' end and the 3' end of the open reading frame sequence of SEQ ID. NO. 4, and

(c) isolating the product of the polymerase chain reaction.

37. (New) An isolated DNA molecule prepared by the process of claim 45.

38. (New) An isolated DNA molecule with a Gax protein comprising an amino acid sequence which is at least 97% identical to the amino acid sequence set forth in SEQ. ID. NO. 2 or the amino acid sequence set forth in SEQ. ID. NO. 4.

39. (New) The DNA molecule of claim 47 wherein said Gax protein is a rat Gax protein and has a molecular weight of from about 30 kDa to about 36 kDa.

40. (New) The DNA molecule of claim 47 wherein said Gax protein is a human Gax protein and has a molecular weight of from about 30 kDa to about 36 kDa.

#### REMARKS

Claims 1-32 are pending in this application. Claims 2-27 are hereby canceled. The specification and claim 1 is amended. Attached hereto is a document entitled "VERSION WITH MARKINGS TO SHOW CHANGES MADE" showing the additions as underlined and the deletions in brackets is attached hereto. New claims 33 to 40 are hereby added.

The specification has been amended to correct typographical errors and to add SEQ. ID. NOS. for the nucleotide sequences and amino acid sequences recited therein. The amendments add no new matter.

The substitute sequence listing which is attached hereto is the same as the computer readable form of the sequence listing which was filed on August 19, 1997, for the parent application. The substitute sequence listing adds no new matter.

Support for amended claim 1 and new claims 39 and 40 is found on page 9, line 10 and/or lines 18-20. Support for new claim 33 is found on page 4, lines 6-8 and 20-22, and page 32, lines 26-30. Support for new claims 34 and 35 is found on page 15, lines 5-17 and Figures 3 and 4. Support for new claims 36 and 37 is found on page 12, lines 30-37 through page 16, lines 1-15, and page 22, lines 17-26. Support for new claims 38-40 is found in Figs 1 and 3 and SEQ ID NO.s 2 and 4.

It is submitted that the amended claims and new claims add no new matter.

Respectfully submitted,

Date:

August 27, 2001

Pamela A. Docherty  
Pamela A. Docherty – Reg. No. 40,591  
(216) 622-8416

VERSION WITH MARKINGS TO SHOW CHANGES MADE

1. (Amended) [A] An isolated DNA [sequence] encoding a mammalian Gax protein [or portion thereof] which inhibits vascular smooth muscle cell proliferation, said Gax protein having a molecular weight of about 30 to 36kDa and comprising a homeodomain, wherein the amino acid sequence of said homeodomain comprises amino acid 185 through amino acid 245 of the amino acid sequence set forth in SEQ. ID. NO. 4.

28. A method for inhibiting the proliferation of eukaryotic cells, comprising the following steps:

- a. providing a nucleic acid sequence encoding a Gax protein, or portion thereof, which inhibits smooth muscle cell proliferation; and
- b. administering said nucleic acid or said protein to the cells.

[illegible]

(1) GENERAL INFORMATION:

(i) APPLICANT: Gorski, David H.  
Walsh, Kenneth

(ii) TITLE OF INVENTION: Growth Arrest Homeobox Gene

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Calfee, Halter, and Griswold  
(B) STREET: 800 Superior Avenue  
(C) CITY: Cleveland  
(D) STATE: Ohio  
(E) COUNTRY: U.S.A.  
(F) ZIP: 44114-2688

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Golrick, Mary E.  
(B) REGISTRATION NUMBER: 34829  
(C) REFERENCE/DOCKET NUMBER: 22311/00114

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (216) 622-8200  
(B) TELEFAX: (216) 241-0816  
(C) TELEX: 980499

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 197..1108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCAAGTGTT TATACGTGCA GGAGACTGGC CGCTCGGCTC AGGACTGGGA TTAGCGGGCT	60
CTGCTCAAAC CCGCGCGGCT TTTACATTAG GAGTGAGTGG GGGAGAGTCC TAGGATTTCT	120
AGTGAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGGAAG	180
CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC	229
Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser	
1 5 10	
CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG	277
Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu	
15 20 25	
GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA	325
Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr	
30 35 40	
TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG	373
Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met	
45 50 55	
TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC CAC CAC CAC CAC	421
Phe Ala Ser Gln His His Arg Gly His His His His His His His His	
60 65 70 75	
CAT CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG	469
His His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp	
80 85 90	
CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT	517
His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu	
95 100 105	
TGC CTG CAG CCT GAT TCC GGA GGG CCC CCG GAG CTG GGG AGC AGC CCT	565
Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro	
110 115 120	
CCG GTC CTG TGC TCC AAC TCT TCT AGC CTG GGC TCC AGC ACC CCG ACC	613
Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr	
125 130 135	
GGA GCC GCG TGC GCA CCA AGG GAT TAT GGC CGT CAA GCG CTG TCA CCC	661
Gly Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro	

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140	145	150	155	
GCA GAA GTG GAG AAG AGA AGT GGC AGC AAA AGA AAA AGC GAC AGT TCA				709
Ala Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser	160	165	170	
GAT TCC CAG GAA GGA AAT TAC AAG TCA GAA GTG AAC AGC AAA CCT AGG				757
Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg	175	180	185	
AGG GAA AGA ACA GCT TTC ACC AAA GAG CAA ATC AGA GAA CTT GAG GCA				805
Arg Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala	190	195	200	
GAG TTC GCC CAT CAT AAC TAT CTG ACC AGA CTG AGA AGA TAT GAG ATA				853
Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile	205	210	215	
GCG GTG AAC CTA GAC CTC ACT GAA AGA CAG GTG AAA GTG TGG TTC CAG				901
Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln	220	225	230	235
AAC AGG AGA ATG AAG TGG AAG CGG GTC AAG GGG GGA CAA CAA GGA GCT				949
Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala	240	245	250	
GCA GCC CGA GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA ACA CTT CTT				997
Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu	255	260	265	
CCA TCA GAG CTG TCA GGA ATT GGT GCA GCC ACC CTC CAG CAG ACA GGG				1045
Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly	270	275	280	
GAC TCA CTA GCA AAT GAC GAC AGT CGC GAT AGT GAC CAC AGC TCT GAG				1093
Asp Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu	285	290	295	
CAC GCA CAC TTA TGATACATAC AGAGACCAGC TCCGTTCTCA GGAAAGCACC				1145
His Ala His Leu	300			
ATTGTGATGG CAAATCTCAC CCAAACATCG TTTACATGGC AGATGACTGT GGCAGTGTTG				1205
CTTAATATAA TTAAACGCAG GCATCTCAAG TCTGTTTCTC ATGATTGATA GAAGGTTTAC				1265
ACTAAGTGCC TCTTATTGAA GATGCTTCCA CAGTGAAATT GGAGAAAGTG AACATATCTA				1325
AATATACTTG TTCCTTATAT GACAGAGAGG GAGATGAATG TTTGCTTTGG CTTGCACTGA				1385
AAATTAAATT GCTACCAAGA GCAAACCTCGG TAAGACATTT TGA CTCAAGT TGTCTCCAGA				1445
GTGAAGATGT TATAGAAATG CTTTGAACAT TCCAGTTGTA CCAGGTCATG TGTGTGACAC				1505

TGGGCAGGTA TTTGCTTTTG CTTGCACTGA AACTTAAACT GCTATCAAGT TAACCCATGA 1565  
AATAGTTTAT CTTGAACAGC CACAGTGCCT GAAATCACCA AGTGGATATA AAATGAACTG 1625  
AAATTCTGTA TATATTACTC CTAAGTCATT TTCCTGTCTT CACTAATTTT AGCAAATGCA 1685  
TTCATATTAG CTGATGAAAA TAGGCTTTCC CGTGGACAAA TGCAGCCAGC TTCTTGTATT 1745  
TTTATACATT TTTTGTGTCAG TCAGAGACAT CAGTATGTGC TTAAGTGTGT TCAAGTAGAG 1805  
GAAATGCAGT AGAGTCTGAT AGGACATATT CTTGGTACCA CAGACAAAAC AAATCTTCTG 1865  
TTGCATTGAC TATCAACTGC TGCAGATACA TTAGAGAACA CACCTAGCCC CCCTCCAGCC 1925  
TCCCTCTGTT ATCGCTCGAA GACATTAGCG TCATAGGCAA GTAGTTACCT TGCCAAATGA 1985  
GTCTTGTGTG GCAGATGTCT GATTTTGTAT CTTTAAACTG TTAATGGTAT GTGTCTGCTT 2045  
CAGTTAACAG GGAAAAAGAT TTCTTCCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA 2105  
CAAAGCTAGT TCTTCAAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA 2165  
AAATACATTA TTTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTTGTAAA 2225  
AAAAAAAGTT AAATAAATG 2244

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	His	Pro	Leu	Phe	Gly	Cys	Leu	Arg	Ser	Pro	His	Ala	Thr	Ala
1				5				10						15	
Gln	Gly	Leu	His	Pro	Phe	Ser	Gln	Ser	Ser	Leu	Ala	Leu	His	Gly	Arg
		20					25						30		
Ser	Asp	His	Met	Ser	Tyr	Pro	Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Cys
		35					40					45			
Ile	Ile	Ala	Gly	Tyr	Pro	Asn	Glu	Glu	Gly	Met	Phe	Ala	Ser	Gln	His
	50					55					60				
His	Arg	Gly	His	His	His	His	His	His	His	His	His	His	His	His	Gln
65					70				75						80
Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	Ser	Asn	Trp	His	Leu	Pro	Gln	Met

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85										90					95				
Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	Leu	Cys	Leu	Gln	Pro	Asp				
			100					105					110						
Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser				
		115					120					125							
Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala				
	130					135					140								
Pro	Arg	Asp	Tyr	Gly	Arg	Gln	Ala	Leu	Ser	Pro	Ala	Glu	Val	Glu	Lys				
145					150					155					160				
Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser	Asp	Ser	Gln	Glu	Gly				
				165					170					175					
Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	Lys	Pro	Arg	Arg	Glu	Arg	Thr	Ala				
			180					185					190						
Phe	Thr	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Glu	Ala	Glu	Phe	Ala	His	His				
		195					200					205							
Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Glu	Ile	Ala	Val	Asn	Leu	Asp				
	210					215					220								
Leu	Thr	Glu	Arg	Gln	Val	Lys	Val	Trp	Phe	Gln	Asn	Arg	Arg	Met	Lys				
225					230					235					240				
Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	Gln	Gly	Ala	Ala	Ala	Arg	Glu	Lys				
				245					250					255					
Glu	Leu	Val	Asn	Val	Lys	Lys	Gly	Thr	Leu	Leu	Pro	Ser	Glu	Leu	Ser				
			260					265					270						
Gly	Ile	Gly	Ala	Ala	Thr	Leu	Gln	Gln	Thr	Gly	Asp	Ser	Leu	Ala	Asn				
		275					280					285							
Asp	Asp	Ser	Arg	Asp	Ser	Asp	His	Ser	Ser	Glu	His	Ala	His	Leu					
	290					295					300								

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 33..941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCTTCTACC TGGAACCCGA AACTTGCATG CT ATG GAA CAC CCG CTC TTT GGC	53
Met Glu His Pro Leu Phe Gly	
1 5	
TGC CTG CGC AGC CCT CAC GCC ACG GCG CAA GGC TTG CAC CCG TTC TCC	101
Cys Leu Arg Ser Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser	
10 15 20	
CAA TCC TCT CTC GCC CTC CAT GGA AGA TCT GAC CAT ATG TCT TAC CCC	149
Gln Ser Ser Leu Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro	
25 30 35	
GAG CTC TCT ACT TCT TCC TCA TCT TGC ATA ATC GCG GGA TAC CCC AAC	197
Glu Leu Ser Thr Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn	
40 45 50 55	
GAA GAG GAC ATG TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC	245
Glu Glu Asp Met Phe Ala Ser Gln His His Arg Gly His His His His	
60 65 70	
CAC CAC CAC CAT CAC CAC CAT CAG CAG CAG CAG CAC CAG GCT CTG CAA	293
His His His His His His His Gln Gln Gln Gln His Gln Ala Leu Gln	
75 80 85	
ACC AAC TGG CAC CTC CCG CAG ATG TCT TCC CCA CCG AGT GCG GCT CGG	341
Thr Asn Trp His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg	
90 95 100	
CAT AGC CTC TGC CTC CAG CCC GAC TCT GGA GGG CCC CCA GAG TTG GGG	389
His Ser Leu Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly	
105 110 115	
AGC AGC CCG CCC GTC CTG TGC TCC AAC TCT TCC AGC TTG GGC TCC AGC	437
Ser Ser Pro Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser	
120 125 130 135	
ACC CCG ACT GGG GCC GCG TGC GCG CCG GGG GAC TAC GGC CGC CAG GCA	485
Thr Pro Thr Gly Ala Ala Cys Ala Pro Gly Asp Tyr Gly Arg Gln Ala	
140 145 150	
CTG TCA CCT GCG GAG GCG GAG AAG CGA AGC GGC GGC AAG AGG AAA AGC	533
Leu Ser Pro Ala Glu Ala Glu Lys Arg Ser Gly Gly Lys Arg Lys Ser	
155 160 165	

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GAC AGC TCA GAC TCC CAG GAA GGA AAT TAC AAG TCA GAA GTC AAC AGC Asp Ser Ser Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser	581
170 175 180	
AAA CCC AGG AAA GAA AGG ACA GCA TTT ACC AAA GAG CAA ATC AGA GAA Lys Pro Arg Lys Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu	629
185 190 195	
CTT GAA GCA GAA TTT GCC CAT CAT AAT TAT CTC ACC AGA CTG AGG CGA Leu Glu Ala Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg	677
200 205 210 215	
TAC GAG ATA GCA GTG AAT CTG GAT CTC ACT GAA AGA CAG GTA AAA GTC Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val	725
220 225 230	
TGG TTC CAA AAC AGG CGG ATG AAG TGG AAG AGG GTA AAG GGT GGA CAG Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln	773
235 240 245	
CAA GGA GCT GCG GCT CGG GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA Gln Gly Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly	821
250 255 260	
ACA CTT CTC CCA TCA GAG CTG TCG GGA ATT GGT GCA GCC ACC CTC CAG Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln	869
265 270 275	
CAA ACA GGG GAC TCT ATA GCA AAT GAA GAC AGT CAC GAC AGT GAC CAC Gln Thr Gly Asp Ser Ile Ala Asn Glu Asp Ser His Asp Ser Asp His	917
280 285 290 295	
AGC TCA GAG CAC GCC CAC CTC TGA Ser Ser Glu His Ala His Leu	941
300	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala	
1 5 10 15	
Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg	
20 25 30	

Ser	Asp	His	Met	Ser	Tyr	Pro	Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Cys	35	40	45
Ile	Ile	Ala	Gly	Tyr	Pro	Asn	Glu	Glu	Asp	Met	Phe	Ala	Ser	Gln	His	50	55	60
His	Arg	Gly	His	His	His	His	His	His	His	His	His	His	His	Gln	Gln	65	70	75
Gln	Gln	His	Gln	Ala	Leu	Gln	Thr	Asn	Trp	His	Leu	Pro	Gln	Met	Ser	85	90	95
Ser	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	Leu	Cys	Leu	Gln	Pro	Asp	Ser	100	105	110
Gly	Gly	Pro	Pro	Glu	Leu	Gly	Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser	Asn	115	120	125
Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala	Pro	130	135	140
Gly	Asp	Tyr	Gly	Arg	Gln	Ala	Leu	Ser	Pro	Ala	Glu	Ala	Glu	Lys	Arg	145	150	155
Ser	Gly	Gly	Lys	Arg	Lys	Ser	Asp	Ser	Ser	Asp	Ser	Gln	Glu	Gly	Asn	165	170	175
Tyr	Lys	Ser	Glu	Val	Asn	Ser	Lys	Pro	Arg	Lys	Glu	Arg	Thr	Ala	Phe	180	185	190
Thr	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Glu	Ala	Glu	Phe	Ala	His	His	Asn	195	200	205
Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Glu	Ile	Ala	Val	Asn	Leu	Asp	Leu	210	215	220
Thr	Glu	Arg	Gln	Val	Lys	Val	Trp	Phe	Gln	Asn	Arg	Arg	Met	Lys	Trp	225	230	235
Lys	Arg	Val	Lys	Gly	Gly	Gln	Gln	Gly	Ala	Ala	Ala	Arg	Glu	Lys	Glu	245	250	255
Leu	Val	Asn	Val	Lys	Lys	Gly	Thr	Leu	Leu	Pro	Ser	Glu	Leu	Ser	Gly	260	265	270
Ile	Gly	Ala	Ala	Thr	Leu	Gln	Gln	Thr	Gly	Asp	Ser	Ile	Ala	Asn	Glu	275	280	285
Asp	Ser	His	Asp	Ser	Asp	His	Ser	Ser	Glu	His	Ala	His	Leu			290	295	300

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AARATWTGGT TYCARAAYMG WMGWATGAA

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20250729 15:45:50

TCAWARRTGW GCRTGYTC

18

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGCAGAT CTCACTGAAA GACAGGTAAA

30

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTTACCTGTC TTTCAGTGAG

20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO



(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCGCAGAT CTAGATTCAC TGCTATCTCG TA

32

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGCGTGCCC CCTCTGATGC TGGCTGGCAA ACATGT

36

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGCGCTCTT GAAGGGCGAG AGAGGATTGG GA

32

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG

38

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGACTTCC AAGGTCTTAG CTATCACTTA AGCAC

35

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGCGCGTCG ACGAACACCC CCTCTTTGGC

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCGCAAGC TTTCATAAGT GTGCGTGCTC

30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCGCGCGGC TTTTACATTA GGAGT

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGGCAAAC ATGCCCTCCT CATTG

25

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGATGGCATG GACTGTGGTC ATGA

24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGATGGCATG GACTGTGGTC ATGA

24